Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (Currently amended) A method for the analysis of ~~cytosine methylation, characterized in that~~ methylated DNA as compared to background DNA of the same sequence but another methylation pattern comprising:

a) converting the DNA to be investigated ~~is~~ chemically or enzymatically ~~converted~~ so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base pairing behavior,

b) hybridizing the converted DNA ~~is hybridized~~ with oligonucleotides, whereby the background DNA ~~of one methylation status~~ forms hybrids with erroneous base pairings~~, while the DNA of the other methylation status forms hybrids without erroneous base pairings or does not form hybrids~~,

c) cleaving the DNA ~~one~~ strand of the erroneously paired hybrids ~~is~~ enzymatically ~~cleaved~~,

d) amplifying the uncleaved DNA,

e) detecting the ~~uncleaved DNA or the cleaved fragments are detected~~ amplificates,

~~e~~f) concluding the methylation status of the investigated DNA ~~is concluded~~ from the detection signal generated in step ~~d~~e),

g) wherein steps b) through d) are conducted simultaneously.

2. (Canceled)

3. (Canceled)

4. (Canceled)

5. (Canceled)

6. (Currently amended) The method according to claim ~~5~~ 1, ~~further characterized in that~~ wherein the background DNA forms several erroneous base pairings with the oligonucleotides.

7. (Currently amended) The method according to claim ~~5~~ 1, ~~further characterized in that~~ wherein the oligonucleotides utilized in step b) are ~~simultaneously~~ also utilized as primers or probes in a later amplification step.

8. (Canceled)

9. (Currently amended) The method according to claim ~~8~~ 1, ~~further characterized in that~~ wherein the amplification or the detection of the amplificates is carried out in a methylation-specific manner.

10. (Currently amended) The method according to claim ~~8~~ 1, ~~further characterized in that~~ wherein said amplifying step comprises amplifying several fragments ~~are~~ simultaneously ~~amplified~~.

11. (Currently amended) The method according to claim 1, ~~further characterized in that~~ wherein the detection in step ~~d~~e) is made by means of a microarray.

12. (Currently amended) The method according to claim 1, ~~further characterized in that~~ ~~in~~ wherein said cleaving step of step c) comprises utilizing a DNA repair enzyme ~~are utilized~~.

13. (Currently amended) The method according to claim 12, ~~further characterized in that~~ wherein said DNA repair enzyme is selected from the group consisting of Mut Y, Mug protein, DNA glycosylase and TDG enzyme.

14. (Currently amended) The method according to claim 12, ~~further characterized in that~~ wherein said DNA repair enzyme is heat-stable ~~enzymes are utilized~~.

15. (Currently amended) The method according to claim 13, ~~further characterized in that a~~ wherein the TDG enzyme is heat-stable ~~TDG enzyme is utilized~~.

16. (Canceled)

17. (Currently amended) ~~The~~ A method ~~according to claim 1~~ for the diagnosis or prognosis of cancer disorders or other diseases associated with a change in the cytosine methylation status, for predicting undesired drug interactions, for establishing a specific drug therapy, for monitoring the success of a drug therapy, for distinguishing cell types or tissues and for investigating cell differentiation, said method comprising the steps of:

a) converting the DNA to be investigated chemically or enzymatically so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base pairing behavior,

b) hybridizing the converted DNA with oligonucleotides, whereby the background DNA forms hybrids with erroneous base pairings,

c) cleaving the DNA strand of the erroneously paired hybrids enzymatically,

d) amplifying the uncleaved DNA,

e) detecting the amplificates,

f) using the detection signal generated in step e) to obtain a diagnosis or prognosis of cancer disorders or other diseases associated with a change in the cytosine methylation status, to predict undesired drug interactions, to establish a specific drug therapy, to monitor the success of a drug therapy, to distinguish cell types or tissues and to investigate cell differentiation,

g) wherein steps b) through d) are conducted simultaneously.

18. (Currently amended) ~~The~~ A method ~~according to claim 1~~ for the early diagnosis of cancer disorders or other diseases associated with a change in the cytosine methylation status comprising the steps of

a) converting the DNA to be investigated chemically or enzymatically so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base pairing behavior,

b) hybridizing the converted DNA with oligonucleotides, whereby the background DNA forms hybrids with erroneous base pairings,

c) cleaving the DNA strand of the erroneously paired hybrids enzymatically,

d) amplifying the uncleaved DNA,

e) detecting the amplificates,

f) using the detection signal generated in step e) for the early diagnosis of cancer disorders or other diseases associated with a change in the cytosine methylation status,

g) wherein steps b) through d) are conducted simultaneously.

19. (Currently amended) The method according to claim 1 ~~wherein~~ further comprising the step of isolating the DNA to be investigated ~~has been isolated~~ from a body fluid sample of an

individual.

20. (Currently amended) The method according to claim 1 ~~wherein~~ further comprising the step of isolating the DNA to be investigated ~~has been isolated~~ from a serum, plasma, sperm, urine or stool sample of an individual.

21. (Canceled)

22. (Canceled)

23. (Canceled)